

## EXHIBIT A

ClustalW (v1.4) multiple sequence alignment

1. huLGR8-A vs. huLGR8-B

Aligned Length = 754    Gaps = 1  
Identities = 729 (96%)    Similarities = 0 (0%)

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huLGR8-A   1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMTTPSCQKGYF   50
huLGR8-B   1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMTTPSCQKGYF   50
*****

huLGR8-A   51 PCGNLTKCLPRAFHCDGKDDCGNGADEENCGDTS GWATIFGTVHGNANSV  100
huLGR8-B   51 PCGNLTKCLPRAFHCDGKDDCGNGADEENCGDTS GWATIFGTVHGNANSV  100
*****

huLGR8-A  101 ALTQECFLKQYPQCCDCKETELEC VNGDLKSVPMISNNVTLLSLKKNKIH  150
huLGR8-B  101 ALTQECFLKQYPQCCDCKETELEC VNGDLKSVPMISNNVTLLSLKKNKIH  150
*****

huLGR8-A  151 SLPDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILYLNHNCITTL  200
huLGR8-B  151 SLPDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILYLNHNCITTL  200
*****

huLGR8-A  201 RPGIFKDLHQLTWLILDDNPITRISQRLFTGLNSLFFLSMVNNYLEALPK  250
huLGR8-B  201 RPGIFKDLHQLTWLILDDNPITRISQRLFTGLNSLFFLSMVNNYLEALPK  250
*****

huLGR8-A  251 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKT  300
huLGR8-B  251 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLDL-----  288
***** *

huLGR8-A  301 FSSLKNLGELDLSSNTITELSPHLFKDLKLLQKLNLSNPLMYLHKNQFE  350
huLGR8-B  289 -----SSNTITELSPHLFKDLKLLQKLNLSNPLMYLHKNQFE  326
*****

huLGR8-A  351 SLKQLQSLDLERIEIPNINTRMFQPMKNLSHIYFKNFRYCSYAPHVRICM  400
huLGR8-B  327 SLKQLQSLDLERIEIPNINTRMFQPMKNLSHIYFKNFRYCSYAPHVRICM  376
*****

huLGR8-A  401 PLTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRSFIKAENTTH  450
huLGR8-B  377 PLTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRSFIKAENTTH  426
*****

huLGR8-A  451 AMSIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGF  500
huLGR8-B  427 AMSIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGF  476
*****

huLGR8-A  501 LAMLSTEVSVLLLTYLTLEKFLVIVFPFSNIRPGKRQTSVILICIWMAGF  550
huLGR8-B  477 LAMLSTEVSVLLLTYLTLEKFLVIVFPFSNIRPGKRQTSVILICIWMAGF  526
*****

huLGR8-A  551 LIAVIPFWNKDYFGNFYKGKNGVCFLYYDQTEDIGSKGYSLGIFLGVNLL  600
huLGR8-B  527 LIAVIPFWNKDYFGNFYKGKNGVCFLYYDQTEDIGSKGYSLGIFLGVNLL  576
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huLGR8-A 601 AFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDAIC 650
huLGR8-B 577 AFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDAIC 626
*****

huLGR8-A 651 WIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKD 700
huLGR8-B 627 WIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKD 676
*****

huLGR8-A 701 KLKQLLHKHQKRSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIM 750
huLGR8-B 677 KLKQLLHKHQKRSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIM 726
*****

huLGR8-A 751 KPVS 754
huLGR8-B 727 KPVS 730
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